

Application Serial No. 10/655,762  
Office Action Mailed January 17, 2006  
Amendment Dated, May 17, 2006

### Listing of Claims

This listing of claims will replace all prior versions and listings of claims in the application.

1. (CURRENTLY AMENDED) A method for measuring the amount of a target nucleic acid sequence in a biological sample, comprising the steps of:
  - a) preparing a sample by adding a known amount of a standard nucleic acid, wherein said standard nucleic acid has having a nucleotide sequence that is at least one base different than the target nucleic acid sequence to a biological specimen containing the target nucleic acid, thereby creating a site of differentiation between the target and the standard nucleic acid;
  - b) amplifying the sample of step a);
  - c) ~~enhancing~~ using a further method to enhance the difference between the standard and the target nucleic acid sequence at the site of differentiation resulting in enhanced products so that the difference created by the at least one base between the standard and the target nucleic acid can be detected; and
  - d) quantifying the enhanced products of step c) by measuring the ratio of the amplified target nucleic acid to the amplified standard nucleic acid to measure the amount of target nucleic acid sequence present in the biological sample.
2. (ORIGINAL) The method of claim 1, wherein the target nucleic acid is from an infectious agent.
3. (ORIGINAL) The method of claim 1, wherein the target nucleic acid is an mRNA transcript.
4. (CURRENTLY AMENDED) The method of claim 1, wherein the quantifying is performed using ~~MALDI-TOF~~ mass spectrometry.
5. (ORIGINAL) The method of claim 1, wherein step c) is performed using primer extension at the site of differentiation.
6. (CURRENTLY AMENDED) The method of claim 1, wherein step c) is performed using ~~allele-specific~~ an enzyme that specifically cleaves ~~cleavage at~~ the site of differentiation.

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7. (ORIGINAL) The method of claim 1, wherein step c) is performed using allele-specific hybridization at the site of differentiation.
8. (CURRENTLY AMENDED) The method of claim 1, 5, 6, ~~and~~ or 7, wherein the quantifying is performed using MALDI-TOF mass spectrometry.
9. (CANCELLED)